In the Specification

Please amend the specification to read as follows:

Please replace the paragraph beginning at page 5, line 35, with the following rewritten paragraph:

C1

Figure 6a and 6b show the cDNA (SEQ ID NO:5) and predicted amino acid sequence of rat testicular FSH-R (SEQ ID NO:6 and SEQ ID NO:7). Amino acid numbering begins at the N-terminal sequence for the predicted mature receptor protein (SEQ ID NO:7), with negative numbers denoting the signal sequence.

Please replace the paragraph beginning at page 5, line 38, with the following rewritten paragraph:

C2

Figure 7 shows structural comparison between the gonadotropin receptors. A) Sequence similarities of receptor domains. The N-terminal half representing the extracellular domain is subdivided into 14 imperfectly duplicated units of approximately 20 residues each and the C-terminal half shows the seven transmembrane segments. Potential glycosylation sites are indicated by filled squares. Different shadings of grey indicate the degrees of sequence conservation for different receptor areas. B) Sequence comparison of receptors in the one letter code. The FSH-R sequence (SEQ ID NO. 7) is shown as the lower sequence and differences as well as substitutions in the LH/CG-R (SEQ ID NO. 3) are presented above. Dots denote insertions introduced for optimal alignment. The extracellular repeats are numbered and demarked by vertical lines. Conserved cysteine residues in the extracellular domain are denoted by filled ovals. Transmembrane regions TMI-TMVII are boxed. Small arrows indicate conserved cysteine residues in the second and third extracellular loops of the receptor.

Please replace the paragraph beginning at page 53, line 35, with the following rewritten paragraph:

Polyadenylated RNA isolated from rat testicular Sertoli cells was used as a template for reverse transcriptase. The resulting cDNA served for the construction of a library in lgt10. An aliquot (1x106 clones) was screened for clones with sequence similarity to two probes derived from the LH/CG-R cDNA (nucleotides 1-483 and 1499-2604). Several positive clones were isolated and cloned cDNAs sequenced as described in F. Sanger et al., Proc. Natl. Acad. Sci. USA, 74:5463-5467 (1977) after subcloning into M13 vectors (J. Vieira and J. Messing, Meth Enzymol., 153:3-11 (1987)). The nucleotide (SEQ ID NO:5) and predicted amino acid sequences (SEQ ID NO:6 and SEQ ID NO:7) of this receptor are shown in Figure 6.

C3

Please replace the paragraph beginning at page 54, line 4, with the following rewritten paragraph:

The translation initiation codon at position 1 defines the start of a 2076 nucleotide open reading frame specifying an N-terminal 17 residue signal sequence followed by a largely hydrophilic domain of 348 residues of putatively extracellular location. This domain contains three N-linked glycosylation sites. It is followed by a structure of 264 residues which comprises seven transmembrane segments. These segments are the hallmark of G protein-coupled receptors. Similar to other such receptors, the 63 residue C-terminus of the FSH-R is proposed to be located intracellularly and contains several amino acids (Ser, Thr, Tyr) whose phosphorylation may regulate receptor activity (K. Palczewski et al., Biochemistry, 27:2306-2313 (1988); J.L. Benovic et al., Proc. Natl. Acad. Sci. USA, 83:2797-2801 (1986)). However, these residues are not part of consensus phosphorylation sites as in other receptors. The mature FSH-R (SEQ ID NO:7) is predicted to comprise 675 amino acids (75K mol. wt.) and to constitute an integral membrane glycoprotein.

C4

Please replace the paragraph beginning at page 54, line 18, with the following rewritten paragraph:

It is illuminating regarding the proposed similarities in function to compare the gonadotropin receptors FSH-R and LH/CG-R (SEQ ID NOS:7 and 3, respectively) (Figure 7). Both molecules are of similar size and display the same structural design. On the level of primary structure, the extracellular domains share approximately 50% sequence similarity while the domains defined by the seven transmembrane segments display 80% sequence identity. The areas of highest sequence divergence comprise the N-terminus, a 40 residue region preceding the first transmembrane segment and the 30 residues encompassing the C-terminus.